



IFWO

## RAW SEQUENCE LISTING

DATE: 08/31/2004

PATENT APPLICATION: US/10/718,933

TIME: 12:19:11

Input Set : N:\Crf3\RULE60\10718933.raw

Output Set: N:\CRF4\08312004\J718933.raw

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1 <110> APPLICANT: Yon, Jeffrey, R
2     Grantham, Christopher J
3     Groot-Kormelink, Paulus J
4 <120> TITLE OF INVENTION: Nicotinic Acetylcholine Receptor
5 <130> FILE REFERENCE: JAB 1529 USA
6 <140> CURRENT APPLICATION NUMBER: US/10/718,933
7 <141> CURRENT FILING DATE: 2003-11-20
8 <150> PRIOR APPLICATION NUMBER: US/09/661,812
9 <151> PRIOR FILING DATE: 2000-09-14
10 <150> PRIOR APPLICATION NUMBER: US 60/153,948
11 <151> PRIOR FILING DATE: 1999-09-15
12 <150> PRIOR APPLICATION NUMBER: GB 0002431.5
13 <151> PRIOR FILING DATE: 2000-02-02
14 <160> NUMBER OF SEQ ID NOS: 24
15 <170> SOFTWARE: PatentIn version 3.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 1299
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
20 <220> FEATURE:
21 <221> NAME/KEY: CDS
22 <222> LOCATION: (1)..(1299)
23 <400> SEQUENCE: 1
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26     Val Glu Thr Glu Cys Leu Gly Ala Glu Gly Arg Leu Ala Leu Lys Leu
27         1             5             10             15
28     ttc cgt gac ctc ttt gcc aac tac aca agt gcc ctg aga cct gtg gca      96
29     Phe Arg Asp Leu Phe Ala Asn Tyr Thr Ser Ala Leu Arg Pro Val Ala
30         20             25             30
31     gac aca gac cag act ctg aat gtg acc ctg gag gtg aca ctg tcc cag      144
32     Asp Thr Asp Gln Thr Leu Asn Val Thr Leu Glu Val Thr Leu Ser Gln
33         35             40             45
34     atc atc gac atg gat gaa cgg aac cag gtg ctg acc ctg tat ctg tgg      192
35     Ile Ile Asp Met Asp Glu Arg Asn Gln Val Leu Thr Leu Tyr Leu Trp
36         50             55             60
37     ata cgg cag gag tgg aca gat gcc tac cta cga tgg gac ccc aat gcc      240
38     Ile Arg Gln Glu Trp Thr Asp Ala Tyr Leu Arg Trp Asp Pro Asn Ala
39         65             70             75             80
40     tat ggt ggc ctg gat gcc atc cgc atc ccc agc agt ctt gtg tgg cgg      288
41     Tyr Gly Gly Leu Asp Ala Ile Arg Ile Pro Ser Ser Leu Val Trp Arg
42         85             90             95
43     cca gac atc gta ctc tat aac aaa gcc gac gcg cag cct cca ggt tcc      336
44     Pro Asp Ile Val Leu Tyr Asn Lys Ala Asp Ala Gln Pro Pro Gly Ser

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ENTERED

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45		100		105		110		
46	gcc	agc	acc	aac	gtg	gtc	ctg	cgc
47	Ala	Ser	Thr	Asn	Val	Val	Leu	Arg
48			115				120	
49	gcg	ccg	gcc	atc	acg	cgc	agc	tcg
50	Ala	Pro	Ala	Ile	Thr	Arg	Ser	Cys
51			130				135	
52	ccg	ttc	gac	gcc	cag	cac	tgc	ggc
53	Pro	Phe	Asp	Ala	Gln	His	Cys	Gly
54			145				150	
55	ggc	ggg	cac	caa	ctg	gat	gtg	cgg
56	Gly	Gly	His	Gln	Leu	Asp	Val	Arg
57							165	
58	gcg	gac	ttc	gtg	gag	aac	gtg	gag
59	Ala	Asp	Phe	Val	Glu	Asn	Val	Glu
60							180	
61	cgg	cgg	cgc	gtg	ctc	acc	tac	ggc
62	Arg	Arg	Arg	Val	Leu	Thr	Tyr	Gly
63							195	
64	gtc	acc	ttc	acg	ctg	ctg	ctg	cgc
65	Val	Thr	Phe	Thr	Leu	Leu	Leu	Arg
66							210	
67	aac	ctg	ctg	ctg	ccc	tgc	gtg	ctc
68	Asn	Leu	Leu	Leu	Pro	Cys	Val	Leu
69							225	
70	ttc	cac	ctg	cct	gcc	gac	tca	ggc
71	Phe	His	Leu	Pro	Ala	Asp	Ser	Gly
72							245	
73	gtg	ctg	ctg	gcg	ctc	acc	gtc	ttc
74	Val	Leu	Leu	Ala	Leu	Thr	Val	Phe
75							260	
76	cca	ccg	gcc	gag	agc	gtg	ccg	ctc
77	Pro	Pro	Ala	Glu	Ser	Val	Pro	Leu
78							275	
79	atg	acc	atg	gtc	aca	ttc	tca	aca
80	Met	Thr	Met	Val	Thr	Phe	Ser	Thr
81							290	
82	ctg	cat	tac	tgt	ggg	ccc	agt	gtc
83	Leu	His	Tyr	Cys	Gly	Pro	Ser	Val
84							305	
85	gcc	ctc	ctg	ctg	gga	cac	ctg	gca
86	Ala	Leu	Leu	Leu	Gly	His	Leu	Ala
87							325	
88	ggg	gag	ccc	tgt	ggg	cag	tcc	agg
89	Gly	Glu	Pro	Cys	Gly	Gln	Ser	Arg
90							340	
91	cag	tcg	cct	gaa	gga	ggg	gct	ggc
92	Gln	Ser	Pro	Glu	Gly	Gly	Ala	Gly
93							355	

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94   cca cga tgt ctg tgc cgc cag gaa gcc cta ctg cac cac gta gcc acc 1152
95   Pro Arg Cys Leu Cys Arg Gln Glu Ala Leu Leu His His Val Ala Thr
96       370               375               380
97   att gcc aat acc ttc cgc agc cac cga gct gcc cag cgc tgc cat gag 1200
98   Ile Ala Asn Thr Phe Arg Ser His Arg Ala Ala Gln Arg Cys His Glu
99       385               390               395               400
100  gac tgg aag cgc ctg gcc cgt gtg atg gac cgc ttc ttc ctg gcc atc 1248
101  Asp Trp Lys Arg Leu Ala Arg Val Met Asp Arg Phe Phe Leu Ala Ile
102              405               410               415
103  ttc ttc tcc atg gcc ctg gtc atg agc ctc ctg gtg ctg gtg cag gcc 1296
104  Phe Phe Ser Met Ala Leu Val Met Ser Leu Leu Val Leu Val Gln Ala
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106  ctg 1299
107  Leu
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110 <211> LENGTH: 433
111 <212> TYPE: PRT
112 <213> ORGANISM: Homo Sapiens
113 <400> SEQUENCE: 2
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117      20               25               30
118  Asp Thr Asp Gln Thr Leu Asn Val Thr Leu Glu Val Thr Leu Ser Gln
119      35               40               45
120  Ile Ile Asp Met Asp Glu Arg Asn Gln Val Leu Thr Leu Tyr Leu Trp
121      50               55               60
122  Ile Arg Gln Glu Trp Thr Asp Ala Tyr Leu Arg Trp Asp Pro Asn Ala
123      65               70               75               80
124  Tyr Gly Gly Leu Asp Ala Ile Arg Ile Pro Ser Ser Leu Val Trp Arg
125      85               90               95
126  Pro Asp Ile Val Leu Tyr Asn Lys Ala Asp Ala Gln Pro Pro Gly Ser
127      100              105              110
128  Ala Ser Thr Asn Val Val Leu Arg His Asp Gly Ala Val Arg Trp Asp
129      115              120              125
130  Ala Pro Ala Ile Thr Arg Ser Ser Cys Arg Val Asp Val Ala Ala Phe
131      130              135              140
132  Pro Phe Asp Ala Gln His Cys Gly Leu Thr Phe Gly Ser Trp Thr His
133      145              150              155              160
134  Gly Gly His Gln Leu Asp Val Arg Pro Arg Gly Ala Ala Ala Ser Leu
135      165              170              175
136  Ala Asp Phe Val Glu Asn Val Glu Trp Arg Val Leu Gly Met Pro Ala
137      180              185              190
138  Arg Arg Arg Val Leu Thr Tyr Gly Cys Cys Ser Glu Pro Tyr Pro Asp
139      195              200              205
140  Val Thr Phe Thr Leu Leu Leu Arg Arg Arg Ala Ala Ala Tyr Val Cys
141      210              215              220
142  Asn Leu Leu Leu Pro Cys Val Leu Ile Ser Leu Leu Ala Pro Leu Ala
143      225              230              235              240

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144	Phe His Leu Pro Ala Asp Ser Gly Glu Lys Val Ser Leu Gly Val Thr	
145		245 250 255
146	Val Leu Leu Ala Leu Thr Val Phe Gln Leu Leu Leu Ala Glu Ser Met	
147		260 265 270
148	Pro Pro Ala Glu Ser Val Pro Leu Ile Gly Lys Tyr Tyr Met Ala Thr	
149		275 280 285
150	Met Thr Met Val Thr Phe Ser Thr Ala Leu Thr Ile Leu Ile Met Asn	
151		290 295 300
152	Leu His Tyr Cys Gly Pro Ser Val Arg Pro Val Pro Ala Trp Ala Arg	
153		305 310 315 320
154	Ala Leu Leu Leu Gly His Leu Ala Arg Gly Leu Cys Val Arg Glu Arg	
155		325 330 335
156	Gly Glu Pro Cys Gly Gln Ser Arg Pro Pro Glu Leu Ser Pro Ser Pro	
157		340 345 350
158	Gln Ser Pro Glu Gly Gly Ala Gly Pro Pro Ala Gly Pro Cys His Glu	
159		355 360 365
160	Pro Arg Cys Leu Cys Arg Gln Glu Ala Leu Leu His His Val Ala Thr	
161		370 375 380
162	Ile Ala Asn Thr Phe Arg Ser His Arg Ala Ala Gln Arg Cys His Glu	
163		385 390 395 400
164	Asp Trp Lys Arg Leu Ala Arg Val Met Asp Arg Phe Phe Leu Ala Ile	
165		405 410 415
166	Phe Phe Ser Met Ala Leu Val Met Ser Leu Leu Val Leu Val Gln Ala	
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168	Leu	
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175	<221> NAME/KEY: CDS	
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179		Met Gly Leu Arg Ser His His
180		1 5
181	ctc agc ctg ggc ctt ctg ctt ctg ttt cta ctc cct gca gag tgc ctg	102
182	Leu Ser Leu Gly Leu Leu Leu Leu Phe Leu Leu Pro Ala Glu Cys Leu	
183		10 15 20
184	gga gct gag ggc cgg ctg gct ctc aag ctg ttc cgt gac ctc ttt gcc	150
185	Gly Ala Glu Gly Arg Leu Ala Leu Lys Leu Phe Arg Asp Leu Phe Ala	
186		25 30 35
187	aac tac aca agt gcc ctg aga cct gtg gca gac aca gac cag act ctg	198
188	Asn Tyr Thr Ser Ala Leu Arg Pro Val Ala Asp Thr Asp Gln Thr Leu	
189		40 45 50 55
190	aat gtg acc ctg gag gtg aca ctg tcc cag atc atc gac atg gat gaa	246
191	Asn Val Thr Leu Glu Val Thr Leu Ser Gln Ile Ile Asp Met Asp Glu	
192		60 65 70
193	cgg aac cag gtg ctg acc ctg tat ctg tgg ata cgg cag gag tgg aca	294

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194	Arg Asn Gln Val Leu Thr Leu Tyr Leu Trp Ile Arg Gln Glu Trp Thr	
195	75 80 85	
196	gat gcc tac cta cga tgg gac ccc aat gcc tat ggt ggc ctg gat gcc	342
197	Asp Ala Tyr Leu Arg Trp Asp Pro Asn Ala Tyr Gly Gly Leu Asp Ala	
198	90 95 100	
199	atc cgc atc ccc agc agt ctt gtg tgg cgg cca gac atc gta ctc tat	390
200	Ile Arg Ile Pro Ser Ser Leu Val Trp Arg Pro Asp Ile Val Leu Tyr	
201	105 110 115	
202	aac aaa gcc gac gcg cag cct cca ggt tcc gcc agc acc aac gtg gtc	438
203	Asn Lys Ala Asp Ala Gln Pro Pro Gly Ser Ala Ser Thr Asn Val Val	
204	120 125 130 135	
205	ctg cgc cac gat ggc gcc gtg cgc tgg gac gcg ccg gcc atc acg cgc	486
206	Leu Arg His Asp Gly Ala Val Arg Trp Asp Ala Pro Ala Ile Thr Arg	
207	140 145 150	
208	agc tcg tgc cgc gtg gat gta gca gcc ttc ccg ttc gac gcc cag cac	534
209	Ser Ser Cys Arg Val Asp Val Ala Ala Phe Pro Phe Asp Ala Gln His	
210	155 160 165	
211	tgc ggc ctg acg ttc ggc tcc tgg act cac ggc ggg cac caa ctg gat	582
212	Cys Gly Leu Thr Phe Gly Ser Trp Thr His Gly Gly His Gln Leu Asp	
213	170 175 180	
214	gtg cgg ccg cgc ggc gct gca gcc agc ctg gcg gac ttc gtg gag aac	630
215	Val Arg Pro Arg Gly Ala Ala Ser Leu Ala Asp Phe Val Glu Asn	
216	185 190 195	
217	gtg gag tgg cgc gtg ctg ggc atg ccg gcg cgg ccg cgc gtg ctc acc	678
218	Val Glu Trp Arg Val Leu Gly Met Pro Ala Arg Arg Arg Val Leu Thr	
219	200 205 210 215	
220	tac ggc tgc tgc tcc gag ccc tac ccc gac gtc acc ttc acg ctg ctg	726
221	Tyr Gly Cys Cys Ser Glu Pro Tyr Pro Asp Val Thr Phe Thr Leu Leu	
222	220 225 230	
223	ctg cgc cgc cgc gcc gcc gcc tac gtg tgc aac ctg ctg ctg ccc tgc	774
224	Leu Arg Arg Arg Ala Ala Ala Tyr Val Cys Asn Leu Leu Leu Pro Cys	
225	235 240 245	
226	gtg ctc atc tcg ctg ctt gcg ccg ctc gcc ttc cac ctg cct gcc gac	822
227	Val Leu Ile Ser Leu Leu Ala Pro Leu Ala Phe His Leu Pro Ala Asp	
228	250 255 260	
229	tca ggc gag aag gtg tcg ctg ggc gtc acc gtg ctg ctg gcg ctc acc	870
230	Ser Gly Glu Lys Val Ser Leu Gly Val Thr Val Leu Leu Ala Leu Thr	
231	265 270 275	
232	gtc ttc cag ttg ctg ctg gcc gag agc atg cca ccg gcc gag agc gtg	918
233	Val Phe Gln Leu Leu Leu Ala Glu Ser Met Pro Pro Ala Glu Ser Val	
234	280 285 290 295	
235	ccg ctc atc ggg aag tac tac atg gcc act atg acc atg gtc aca ttc	966
236	Pro Leu Ile Gly Lys Tyr Tyr Met Ala Thr Met Thr Met Val Thr Phe	
237	300 305 310	
238	tca aca gca ctc acc atc ctt atc atg aac ctg cat tac tgt ggt ccc	1014
239	Ser Thr Ala Leu Thr Ile Leu Ile Met Asn Leu His Tyr Cys Gly Pro	
240	315 320 325	
241	agt gtc cgc cca gtg cca gcc tgg gct agg gcc ctc ctg ctg gga cac	1062
242	Ser Val Arg Pro Val Pro Ala Trp Ala Arg Ala Leu Leu Leu Gly His	

RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 08/31/2004  
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Output Set: N:\CRF4\08312004\J718933.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:19; Xaa Pos. 101

Seq#:20; Xaa Pos. 101

**VERIFICATION SUMMARY**

DATE: 08/31/2004

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TIME: 12:19:12

Input Set : N:\Crf3\RULE60\10718933.raw

Output Set: N:\CRF4\08312004\J718933.raw

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:691 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19  
:718 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:19  
:718 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:751  
:750 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 19  
:844 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:96